

Arne O Smalås

List of Publications by Year in descending order

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72
papers

2,300
citations

201674

27
h-index

223800

46
g-index

72
all docs

72
docs citations

72
times ranked

2015
citing authors

#	ARTICLE	IF	CITATIONS
1	Features and structure of a cold active N-acetylneuraminase lyase. PLoS ONE, 2019, 14, e0217713.	2.5	5
2	Draft Genome Sequence of the Symbiotically Competent Cyanobacterium <i>Nostoc</i> sp. Strain KVJ20. Microbiology Resource Announcements, 2019, 8, .	0.6	1
3	Structural and functional characterization of two unusual endonuclease III enzymes from <i>Deinococcus radiodurans</i> . Journal of Structural Biology, 2015, 191, 87-99.	2.8	20
4	Characterization of the N-acetylneuraminic acid synthase (NeuB) from the psychrophilic fish pathogen <i>Moritella viscosa</i> . Carbohydrate Research, 2015, 402, 133-145.	2.3	10
5	Structural and biophysical analysis of interactions between cod and human uracil-DNA N-glycosylase (UNG) and UNG inhibitor (Ugi). Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2093-2100.	2.5	6
6	High quality draft genome sequence of <i>Streptomyces</i> sp. strain AW19M42 isolated from a sea squirt in Northern Norway. Standards in Genomic Sciences, 2014, 9, 676-686.	1.5	5
7	Characterization of the sialic acid synthase from <i>Aliivibrio salmonicida</i> suggests a novel pathway for bacterial synthesis of 7-O-acetylated sialic acids. Glycobiology, 2013, 23, 806-819.	2.5	7
8	Presence of acyl-ε-homoserine lactones in 57 members of the <i>Vibrionaceae</i> family. Journal of Applied Microbiology, 2013, 115, 835-847.	3.1	46
9	Draft Genome Sequence of the Actinomycete <i>Rhodococcus</i> sp. Strain AW25M09, Isolated from the Hadsel Fjord, Northern Norway. Genome Announcements, 2013, 1, e0005513.	0.8	8
10	Thermal unfolding studies of cold adapted uracil-DNA N-glycosylase (UNG) from Atlantic cod (<i>Gadus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Biochemistry and Molecular Biology, 2012, 161, 60-68.	1.6	10
11	Structure of uracil-DNA N-glycosylase (UNG) from <i>Vibrio cholerae</i> : mapping temperature adaptation through structural and mutational analysis. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 130-136.	0.7	9
12	Thermodynamics and structure of a salmon cold active goose-type lysozyme. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2010, 156, 254-263.	1.6	7
13	Structure of a highly stable mutant of human fibroblast growth factor 1. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 67-73.	2.5	8
14	Ion pairs and their role in modulating stability of cold- and warm-active uracil DNA glycosylase. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1219-1230.	2.6	8
15	Electrostatic interactions play an essential role in DNA repair and cold-adaptation of Uracil DNA glycosylase. Journal of Molecular Modeling, 2008, 14, 201-213.	1.8	12
16	Structural evidence for lack of inhibition of fish goose-type lysozymes by a bacterial inhibitor of lysozyme. Journal of Molecular Modeling, 2008, 14, 777-788.	1.8	13
17	Structural adaptation of endonuclease I from the cold-adapted and halophilic bacterium <i>Vibrio salmonicida</i> . Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 368-376.	2.5	25
18	Uracil-DNA N-glycosylase (UNG) from the marine, psychrophilic bacterium <i>Vibrio salmonicida</i> shows cold adapted features. Enzyme and Microbial Technology, 2008, 42, 594-600.	3.2	4

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19	Effects of salt on the kinetics and thermodynamic stability of endonuclease I from <i>Vibrio salmonicida</i> and <i>Vibrio cholerae</i> . FEBS Journal, 2008, 275, 1593-1605.	4.7	14
20	Effect of fish skin mucus on the soluble proteome of <i>Vibrio salmonicida</i> analysed by 2-D gel electrophoresis and tandem mass spectrometry. Microbial Pathogenesis, 2007, 42, 36-45.	2.9	44
21	Sequence comparison and environmental adaptation of a bacterial endonuclease. Computational Biology and Chemistry, 2007, 31, 163-172.	2.3	11
22	Comparative unfolding studies of psychrophilic and mesophilic uracil DNA glycosylase: MD simulations show reduced thermal stability of the cold-adapted enzyme. Journal of Molecular Graphics and Modelling, 2007, 26, 124-134.	2.4	19
23	The first structure of a cold-active catalase from <i>Vibrio salmonicida</i> at 1.96 Å... reveals structural aspects of cold adaptation. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 135-148.	2.5	24
24	Comparative studies of endonuclease I from cold-adapted <i>Vibrio salmonicida</i> and mesophilic <i>Vibrio cholerae</i> . FEBS Journal, 2007, 274, 252-263.	4.7	45
25	Free energy calculations show that acidic P1 variants undergo large pKa shifts upon binding to trypsin. Proteins: Structure, Function and Bioinformatics, 2006, 64, 740-748.	2.6	17
26	Probing the Effect of Point Mutations at Protein-Protein Interfaces with Free Energy Calculations. Biophysical Journal, 2006, 90, 433-442.	0.5	59
27	The structure of <i>Vibrio cholerae</i> extracellular endonuclease I reveals the presence of a buried chloride ion. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1387-1391.	2.5	14
28	The 1.8 Å crystal structure of a proteinase K-like enzyme from a psychrotroph <i>Serratia</i> species. FEBS Journal, 2006, 273, 61-71.	4.7	32
29	Predicting proteinase specificities from free energy calculations. Journal of Molecular Graphics and Modelling, 2006, 25, 176-185.	2.4	10
30	The Crystal Structure of Mismatch-specific Uracil-DNA Glycosylase (MUG) from <i>Deinococcus radiodurans</i> Reveals a Novel Catalytic Residue and Broad Substrate Specificity. Journal of Biological Chemistry, 2006, 281, 569-577.	3.4	19
31	Structure of the uracil-DNA-glycosylase (UNG) from <i>Deinococcus radiodurans</i> . Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 1049-1056.	2.5	25
32	Structure-Function Relationships in Serine Protease-Bovine Pancreatic Trypsin Inhibitor Interaction. Protein and Peptide Letters, 2005, 12, 403-407.	0.9	23
33	Increased Flexibility as a Strategy for Cold Adaptation. Journal of Biological Chemistry, 2005, 280, 18042-18048.	3.4	69
34	Trypsin specificity as elucidated by LIE calculations, X-ray structures, and association constant measurements. Protein Science, 2004, 13, 1056-1070.	7.6	75
35	The primary structure and specificity determining residues displayed by recombinant salmon antibody domains. Molecular Immunology, 2004, 40, 1347-1360.	2.2	5
36	Optimisation of the Surface Electrostatics as a Strategy for Cold Adaptation of Uracil-DNA N-glycosylase (UNG) from Atlantic Cod (<i>Gadus morhua</i>). Journal of Molecular Biology, 2004, 343, 1221-1230.	4.2	30

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37	Crystal Structures of Five Bovine Chymotrypsin Complexes with P1 BPTI Variants. <i>Journal of Molecular Biology</i> , 2004, 344, 1005-1020.	4.2	17
38	The structure of uracil-DNA glycosylase from Atlantic cod (<i>Gadus morhua</i>) reveals cold-adaptation features. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1357-1365.	2.5	59
39	Structural Consequences of Accommodation of Four Non-cognate Amino Acid Residues in the S1 Pocket of Bovine Trypsin and Chymotrypsin. <i>Journal of Molecular Biology</i> , 2003, 333, 845-861.	4.2	15
40	The antibody site in Atlantic salmon; phage display and modeling of scFv with anti-hapten binding ability. <i>Developmental and Comparative Immunology</i> , 2002, 26, 201-206.	2.3	13
41	Identification, cloning, and expression of uracil-DNA glycosylase from Atlantic cod (<i>Gadus morhua</i>): characterization and homology modeling of the cold-active catalytic domain. <i>Extremophiles</i> , 2002, 6, 73-86.	2.3	29
42	Computational analysis of binding of P1 variants to trypsin. <i>Protein Science</i> , 2001, 10, 1584-1595.	7.6	47
43	Electrostatic effects play a central role in cold adaptation of trypsin. <i>FEBS Letters</i> , 2001, 499, 171-175.	2.8	38
44	Environmental fate of chlorinated bornanes estimated by theoretical descriptors. <i>Chemosphere</i> , 2001, 43, 665-674.	8.2	8
45	Atomic resolution structures of trypsin provide insight into structural radiation damage. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 488-497.	2.5	71
46	Crystallization and preliminary X-ray diffraction analysis of a cold-adapted uracil-DNA glycosylase from Atlantic cod (<i>Gadus morhua</i>). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1706-1708.	2.5	9
47	Electrostatics of mesophilic and psychrophilic trypsin isoenzymes: Qualitative evaluation of electrostatic differences at the substrate binding site. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 40, 207-217.	2.6	40
48	Structural comparison of psychrophilic and mesophilic trypsins. <i>FEBS Journal</i> , 2000, 267, 1039-1049.	0.2	83
49	Evaluation of protein-protein association energies by free energy perturbation calculations. <i>Protein Engineering, Design and Selection</i> , 2000, 13, 239-245.	2.1	22
50	Substitutions at the P1 position in BPTI strongly affect the association energy with serine proteinases 1. Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 301, 205-217.	4.2	71
51	Cold adapted enzymes. <i>Biotechnology Annual Review</i> , 2000, 6, 1-57.	2.1	200
52	High-resolution structures of three new trypsin-squash-inhibitor complexes: a detailed comparison with other trypsins and their complexes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 139-148.	2.5	30
53	Comparative Molecular Dynamics of Mesophilic and Psychrophilic Protein Homologues Studied by 1.2 ns Simulations. <i>Journal of Biomolecular Structure and Dynamics</i> , 1999, 17, 493-506.	3.5	32
54	The crystal structures of the complexes between bovine β -trypsin and ten P1 variants of BPTI. <i>Journal of Molecular Biology</i> , 1999, 287, 923-942.	4.2	91

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55	Interscaffolding additivity: binding of P 1 variants of bovine pancreatic trypsin inhibitor to four serine proteases 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1999, 289, 175-186.	4.2	111
56	The crystal structure of anionic salmon trypsin in complex with bovine pancreatic trypsin inhibitor. <i>FEBS Journal</i> , 1998, 256, 317-324.	0.2	30
57	Structure of a Non-psychrophilic Trypsin from a Cold-Adapted Fish Species. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 780-798.	2.5	21
58	Temperature and pH sensitivity of trypsins from atlantic salmon (<i>Salmo salar</i>) in comparison with bovine and porcine trypsin. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 1996, 115, 33-45.	1.6	91
59	Refined crystal structure of lysozyme from the rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 354-367.	2.5	6
60	Crystallization and preliminary X-ray crystallographic studies of native elastase from North Atlantic salmon (<i>Salmo salar</i>). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 393-394.	2.5	1
61	Structure of anionic salmon trypsin in a second crystal form. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 725-730.	2.5	5
62	Structure of native pancreatic elastase from North Atlantic salmon at 1.61 Å... resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 925-937.	2.5	28
63	Molecular Cloning and Characterization of Anionic and Cationic Variants of Trypsin from Atlantic Salmon. <i>FEBS Journal</i> , 1995, 232, 677-685.	0.2	80
64	Comparative molecular dynamics simulation studies of salmon and bovine trypsins in aqueous solution. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 379-388.	2.1	19
65	Molecular Cloning and Characterization of Anionic and Cationic Variants of Trypsin from Atlantic Salmon. <i>FEBS Journal</i> , 1995, 232, 677-685.	0.2	4
66	Cold adaption of enzymes: Structural comparison between salmon and bovine trypsins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1994, 20, 149-166.	2.6	146
67	Consideration in the choice of a wavelength range for white-beam Laue diffraction. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1993, 49, 305-307.	2.5	0
68	Structure determination and refinement of benzamidine-inhibited trypsin from the North Atlantic salmon (<i>Salmo salar</i>) at 1.82 Å... resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1993, 49, 318-330.	2.5	7
69	The hydrolytic water molecule in trypsin, revealed by time-resolved Laue crystallography. <i>Science</i> , 1993, 259, 669-673.	12.6	108
70	Response. <i>Science</i> , 1993, 261, 621-622.	12.6	8
71	Laue diffraction as a tool in dynamic studies: hydrolysis of a transiently stable intermediate in catalysis by trypsin. <i>Philosophical Transactions of the Royal Society: Physical and Engineering Sciences</i> , 1992, 340, 285-300.	1.0	6
72	Crystallization and preliminary X-ray crystallographic studies of benzamidine-inhibited trypsin from the north atlantic salmon (<i>Salmo salar</i>). <i>Journal of Molecular Biology</i> , 1990, 214, 355-358.	4.2	15